

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/780, 043 A  
Source: JFW/16  
Date Processed by STIC: 05/04/2006

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IFW16

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/780,043A

DATE: 05/04/2006

TIME: 12:02:58

Input Set : A:\10-780,043.txt

Output Set: N:\CRF4\05042006\J780043A.raw

3 <110> APPLICANT: Bates, Elizabeth  
 4 Fournier, Nathalie  
 5 Chalus, Lionel  
 6 Garrone, Pierre  
 8 <120> TITLE OF INVENTION: MONOCYTE-DERIVED NUCLEIC ACIDS AND RELATED COMPOSITIONS AND  
 9 METHODS  
 11 <130> FILE REFERENCE: SF0977XB  
 13 <140> CURRENT APPLICATION NUMBER: US 10/780,043A  
 14 <141> CURRENT FILING DATE: 2004-02-17  
 16 <150> PRIOR APPLICATION NUMBER: US 09/869,388  
 17 <151> PRIOR FILING DATE: 1999-12-29  
 19 <150> PRIOR APPLICATION NUMBER: US 09/223,919  
 20 <151> PRIOR FILING DATE: 1998-12-31  
 22 <150> PRIOR APPLICATION NUMBER: US 09/224,604  
 23 <151> PRIOR FILING DATE: 1998-12-31  
 25 <160> NUMBER OF SEQ ID NOS: 16  
 27 <170> SOFTWARE: PatentIn version 3.3  
 29 <210> SEQ ID NO: 1  
 30 <211> LENGTH: 1249  
 31 <212> TYPE: DNA  
 32 <213> ORGANISM: Homo sapiens  
 35 <220> FEATURE:  
 36 <221> NAME/KEY: CDS  
 37 <222> LOCATION: (154)..(1062)  
 39 <220> FEATURE:  
 40 <221> NAME/KEY: sig\_peptide  
 41 <222> LOCATION: (154)..(210)  
 43 <220> FEATURE:  
 44 <221> NAME/KEY: mat\_peptide  
 45 <222> LOCATION: (211)..(1062)  
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 50 ctcaccta cccccaggcg gcccctccac agggcccttc tcctgcctgg acggctctgc 120  
 52 tggtctcccc gtccccctgga gaagaacaag gcc atg ggt cgg ccc ctg ctg ctg 174  
 53 Met Gly Arg Pro Leu Leu Leu  
 54 -15  
 56 ccc cta ctg ccc ctg ctg ccg cca gca ttt ctg cag cct agt ggc 222  
 57 Pro Leu Leu Pro Leu Leu Leu Pro Pro Ala Phe Leu Gln Pro Ser Gly  
 58 -10 -5 -1 1  
 60 tcc aca gga tct ggt cca agc tac ctt tat ggg gtc act caa cca aaa 270  
 61 Ser Thr Gly Ser Gly Pro Ser Tyr Leu Tyr Gly Val Thr Gln Pro Lys  
 62 5 10 15 20  
 64 cac ctc tca gcc tcc atg ggt ggc tct gtg gaa atc ccc ttc tcc ttc 318

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65 His Leu Ser Ala Ser Met Gly Gly Ser Val Glu Ile Pro Phe Ser Phe		
66                   25                   30                   35		
68 tat tac ccc tgg gag tta gcc aca gct ccc gac gtg aga ata tcc tgg	366	
69 Tyr Tyr Pro Trp Glu Leu Ala Thr Ala Pro Asp Val Arg Ile Ser Trp		
70                   40                   45                   50		
72 aga cgg ggc cac ttc cac ggg cag tcc ttc tac agc aca agg cgg cct	414	
73 Arg Arg Gly His Phe His Gly Gln Ser Phe Tyr Ser Thr Arg Pro Pro		
74                   55                   60                   65		
76 tcc att cac aag gat tat gtg aac cgg ctc ttt ctg aac tgg aca gag	462	
77 Ser Ile His Lys Asp Tyr Val Asn Arg Leu Phe Leu Asn Trp Thr Glu		
78                   70                   75                   80		
80 ggt cag aag agc ggc ttc ctc agg atc tcc aac ctg cag aag cag gac	510	
81 Gly Gln Lys Ser Gly Phe Leu Arg Ile Ser Asn Leu Gln Lys Gln Asp		
82 85                   90                   95                   100		
84 cag tct gtg tat ttc tgc cga gtt gag ctg gac aca cgg agc tca ggg	558	
85 Gln Ser Val Tyr Phe Cys Arg Val Glu Leu Asp Thr Arg Ser Ser Gly		
86                   105                   110                   115		
88 agg cag cag tgg cag tcc atc gag ggg acc aaa ctc tcc atc acc cag	606	
89 Arg Gln Gln Trp Gln Ser Ile Glu Gly Thr Lys Leu Ser Ile Thr Gln		
90                   120                   125                   130		
92 gct gtc acg acc acc cag agg ccc agc agc atg act acc acc tgg	654	
93 Ala Val Thr Thr Gln Arg Pro Ser Ser Met Thr Thr Thr Trp		
94                   135                   140                   145		
96 agg ctc agt agc aca acc aca acc ggc ctc agg gtc aca cag ggc	702	
97 Arg Leu Ser Ser Thr Thr Thr Thr Gly Leu Arg Val Thr Gln Gly		
98                   150                   155                   160		
100 aaa cga cgc tca gac tct tgg cac ata agt ctg gag act gct gtg ggg	750	
101 Lys Arg Arg Ser Asp Ser Trp His Ile Ser Leu Glu Thr Ala Val Gly		
102 165                   170                   175                   180		
104 gtg gca gtg gct act gtg ctc gga atc atg att ttg gga ctg atc	798	
105 Val Ala Val Ala Val Thr Val Leu Gly Ile Met Ile Leu Gly Leu Ile		
106                   185                   190                   195		
108 tgc ctc ctc agg tgg agg aga agg aaa ggt cag cag cgg act aaa gcc	846	
109 Cys Leu Leu Arg Trp Arg Arg Lys Gly Gln Gln Arg Thr Lys Ala		
110                   200                   205                   210		
112 aca acc cca gcc agg gaa ccc ttc caa aac aca gag gag cca tat gag	894	
113 Thr Thr Pro Ala Arg Glu Pro Phe Gln Asn Thr Glu Glu Pro Tyr Glu		
114                   215                   220                   225		
116 aat atc agg aat gaa gga caa aat aca gat ccc aag cta aat ccc aag	942	
117 Asn Ile Arg Asn Glu Gly Gln Asn Thr Asp Pro Lys Leu Asn Pro Lys		
118                   230                   235                   240		
120 gat gac ggc atc gta tat gct tcc ctt gcc ctc tcc agc tcc acc tca	990	
121 Asp Asp Gly Ile Val Tyr Ala Ser Leu Ala Leu Ser Ser Thr Ser		
122 245                   250                   255                   260		
124 ccc aga gca cct ccc agc cac cgt ccc aag agc ccc cag aac gag	1038	
125 Pro Arg Ala Pro Pro Ser His Arg Pro Leu Lys Ser Pro Gln Asn Glu		
126                   265                   270                   275		
128 acc ctg tac tct gtc tta aag gcc taaccaatgg acagccctct caagactgaa	1092	
129 Thr Leu Tyr Ser Val Leu Lys Ala		

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130           280  
132 tggtagggcc aggtacagtgcgcacacct gtaatcccag ctactctgaa gcctgaggca   1152  
134 gaatcaagtgcgcccaggagttcagggcca gcttgataatggagcgaga tgccatctct   1212  
136 agttaaaaat atatattaac aataaaagtaa caaattt                         1249  
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140 <211> LENGTH: 303  
141 <212> TYPE: PRT  
142 <213> ORGANISM: Homo sapiens  
144 <400> SEQUENCE: 2  
146 Met Gly Arg Pro Leu Leu Leu Pro Leu Leu Pro Leu Leu Pro Pro  
147               -15               -10               -5  
150 Ala Phe Leu Gln Pro Ser Gly Ser Thr Gly Ser Gly Pro Ser Tyr Leu  
151               -1    1            5               10  
154 Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly Gly Ser  
155       15           20           25  
158 Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala Thr Ala  
159 30           35           40           45  
162 Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly Gln Ser  
163       50           55           60  
166 Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val Asn Arg  
167       65           70           75  
170 Leu Phe Leu Asn Trp Thr Glu Gly Gln Lys Ser Gly Phe Leu Arg Ile  
171       80           85           90  
174 Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys Arg Val Glu  
175       95           100          105  
178 Leu Asp Thr Arg Ser Ser Gly Arg Gln Gln Trp Gln Ser Ile Glu Gly  
179 110       115          120          125  
182 Thr Lys Leu Ser Ile Thr Gln Ala Val Thr Thr Thr Gln Arg Pro  
183       130          135          140  
186 Ser Ser Met Thr Thr Trp Arg Leu Ser Ser Thr Thr Thr Thr Thr  
187       145          150          155  
190 Gly Leu Arg Val Thr Gln Gly Lys Arg Arg Ser Asp Ser Trp His Ile  
191       160          165          170  
194 Ser Leu Glu Thr Ala Val Gly Val Ala Val Ala Val Thr Val Leu Gly  
195       175          180          185  
198 Ile Met Ile Leu Gly Leu Ile Cys Leu Leu Arg Trp Arg Arg Arg Lys  
199 190       195          200          205  
202 Gly Gln Gln Arg Thr Lys Ala Thr Thr Pro Ala Arg Glu Pro Phe Gln  
203       210          215          220  
206 Asn Thr Glu Glu Pro Tyr Glu Asn Ile Arg Asn Glu Gly Gln Asn Thr  
207       225          230          235  
210 Asp Pro Lys Leu Asn Pro Lys Asp Asp Gly Ile Val Tyr Ala Ser Leu  
211       240          245          250  
214 Ala Leu Ser Ser Ser Thr Ser Pro Arg Ala Pro Pro Ser His Arg Pro  
215       255          260          265  
218 Leu Lys Ser Pro Gln Asn Glu Thr Leu Tyr Ser Val Leu Lys Ala  
219 270       275          280  
222 <210> SEQ ID NO: 3  
223 <211> LENGTH: 943

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PATENT APPLICATION: US/10/780,043A

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Input Set : A:\10-780,043.txt  
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224 <212> TYPE: DNA  
 225 <213> ORGANISM: Homo sapiens  
 228 <220> FEATURE:  
 229 <221> NAME/KEY: CDS  
 230 <222> LOCATION: (130)..(819)  
 232 <220> FEATURE:  
 233 <221> NAME/KEY: sig\_peptide  
 234 <222> LOCATION: (130)..(180)  
 236 <220> FEATURE:  
 237 <221> NAME/KEY: mat\_peptide  
 238 <222> LOCATION: (181)..(819)  
 240 <400> SEQUENCE: 3  
 241 acagccctct tcggagcctc agcccggttc tccactca cctcaacccc caggcgcccc 60  
 243 ctccacaggg cccctcttgc gctggacgg ctctgctggt ctccccgtcc cctggagaag 120  
 245 aacaaggcc atg ggt egg ccc ctg ctg ccc cta ctg ccc ctg ctg ctg 171  
 246 Met Gly Arg Pro Leu Leu Leu Pro Leu Leu Pro Leu Leu Leu  
 247 -15. -10 -5  
 249 ccg cca gca ttt ctg cag cct agt ggc tcc aca gga tct ggt cca agc 219  
 250 Pro Pro Ala Phe Leu Gln Pro Ser Gly Ser Thr Gly Ser Gly Pro Ser  
 251 -1 T 5 10  
 253 tac ctt tat ggg gtc actcaa cca aaa cac ctc tca gcc tcc atg ggt 267  
 254 Tyr Leu Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly  
 255 15 20 25  
 257 ggc tct gtg gaa atc ccc ttc tcc ttc tat tac ccc tgg gag tta gcc 315  
 258 Gly Ser Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala  
 259 30 35 40 45  
 261 aca gct ccc gac gtg aga ata tcc tgg aga cgg ggc cac ttc cac ggg 363  
 262 Thr Ala Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly  
 263 50 55 60  
 265 cag tcc ttc tac agc aca agg ccc cct tcc att cac aag gat tat gtg 411  
 266 Gln Ser Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val  
 267 65 70 75  
 269 aac cgg ctc ttt ctg aac tgg aca gag ggt cag aag agc ggc ttc ctc 459  
 270 Asn Arg Leu Phe Leu Asn Trp Thr Glu Gly Gln Lys Ser Gly Phe Leu  
 271 80 85 90  
 273 agg atc tcc aac ctg cag aag cag gac cag tct gtg tat ttc tgc cga 507  
 274 Arg Ile Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys Arg  
 275 95 100 105  
 277 gtt gag ctg gac aca cgg agc tca ggg agg cag cag tgg cag tcc atc 555  
 278 Val Glu Leu Asp Thr Arg Ser Ser Gly Arg Gln Gln Trp Gln Ser Ile  
 279 110 115 120 125  
 281 gag ggg acc aaa ctc tcc atc acc cag ggt cag cag cgg act aaa gcc 603  
 282 Glu Gly Thr Lys Leu Ser Ile Thr Gln Gly Gln Gln Arg Thr Lys Ala  
 283 130 135 140  
 285 aca acc cca gcc agg gaa ccc ttc caa aac aca gag gag cca tat gag 651  
 286 Thr Thr Pro Ala Arg Glu Pro Phe Gln Asn Thr Glu Glu Pro Tyr Glu  
 287 145 150 155  
 289 aat atc agg aat gaa gga caa aat aca gat ccc aag cta aat ccc aag 699  
 290 Asn Ile Arg Asn Glu Gly Gln Asn Thr Asp Pro Lys Leu Asn Pro Lys

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291	160	165	170	
293	gat gac ggc atc gtc tat gct tcc ctt gcc ctc tcc agc tcc acc tca			747
294	Asp Asp Gly Ile Val Tyr Ala Ser Leu Ala Leu Ser Ser Ser Thr Ser			
295	175	180	185	
297	ccc aga gca cct ccc agc cac cgt ccc ctc aag agc ccc cag aac gag			795
298	Pro Arg Ala Pro Pro Ser His Arg Pro Leu Lys Ser Pro Gln Asn Glu			
299	190	195	200	205
301	acc ctg tac tct gtc tta aag gcc taaccaatgg acagccctct caagactgaa			849
302	Thr Leu Tyr Ser Val Leu Lys Ala			
303	210			
305	tggtgaggcc aggtacagtgcgcacacct gtaatcccag ctactctgaa gcctgaggca			909
307	gaatcaagtgcgcccaggatcaggcca gctt			943
310	<210> SEQ ID NO: 4			
311	<211> LENGTH: 230			
312	<212> TYPE: PRT			
313	<213> ORGANISM: Homo sapiens			
315	<400> SEQUENCE: 4			
317	Met Gly Arg Pro Leu Leu Leu Pro Leu Leu Pro Leu Leu Pro Pro			
318	-15	-10	-5	
321	Ala Phe Leu Gln Pro Ser Gly Ser Thr Gly Ser Gly Pro Ser Tyr Leu			
322	-1 1	5	10	15
325	Tyr Gly Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly Gly Ser			
326	20	25	30	
329	Val Glu Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala Thr Ala			
330	35	40	45	
333	Pro Asp Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly Gln Ser			
334	50	55	60	
337	Phe Tyr Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val Asn Arg			
338	65	70	75	
341	Leu Phe Leu Asn Trp Thr Glu Gly Gln Lys Ser Gly Phe Leu Arg Ile			
342	80	85	90	95
345	Ser Asn Leu Gln Lys Gln Asp Gln Ser Val Tyr Phe Cys Arg Val Glu			
346	100	105	110	
349	Leu Asp Thr Arg Ser Ser Gly Arg Gln Gln Trp Gln Ser Ile Glu Gly			
350	115	120	125	
353	Thr Lys Leu Ser Ile Thr Gln Gly Gln Gln Arg Thr Lys Ala Thr Thr			
354	130	135	140	
357	Pro Ala Arg Glu Pro Phe Gln Asn Thr Glu Glu Pro Tyr Glu Asn Ile			
358	145	150	155	
361	Arg Asn Glu Gly Gln Asn Thr Asp Pro Lys Leu Asn Pro Lys Asp Asp			
362	160	165	170	175
365	Gly Ile Val Tyr Ala Ser Leu Ala Leu Ser Ser Ser Thr Ser Pro Arg			
366	180	185	190	
369	Ala Pro Pro Ser His Arg Pro Leu Lys Ser Pro Gln Asn Glu Thr Leu			
370	195	200	205	
373	Tyr Ser Val Leu Lys Ala			
374	210			
377	<210> SEQ ID NO: 5			
378	<211> LENGTH: 1450			

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/780,043A

DATE: 05/04/2006

TIME: 12:02:59

Input Set : A:\10-780,043.txt

Output Set: N:\CRF4\05042006\J780043A.raw